

FIG. 1

**BOX 1:**

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Ec	(20)	DGGMGTMIQ	(SEQ ID NO: 3)
Ss	(20)	DGAMGTNLQ	(SEQ ID NO: 4)
Ml2	(5)	DGAMGTQLQ	(SEQ ID NO: 5)
Hi	(20)	DGAMGTMIQ	(SEQ ID NO: 6)
Ce	(22)	DGAMGTMIQ	(SEQ ID NO: 7)
Hs	(34)	DGGMGTMIQ	(SEQ ID NO: 8)

**BOX 2:**

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Ec	(752)	ATVKGDVHDIGKN	(SEQ ID NO: 9)
Ss	(729)	ATVKGDVHDIGKN	(SEQ ID NO:10)
Ml2	(726)	ATVKGDVHDIGKN	(SEQ ID NO:11)
Hi	(142)	ATVKGDVHDIGKN	(SEQ ID NO:12)
Ce	(766)	ATVKGDVHDIGKN	(SEQ ID NO:13)
Hs	(778)	ATVKGDVHDIGKN	(SEQ ID NO:14)

**BOX 3:**

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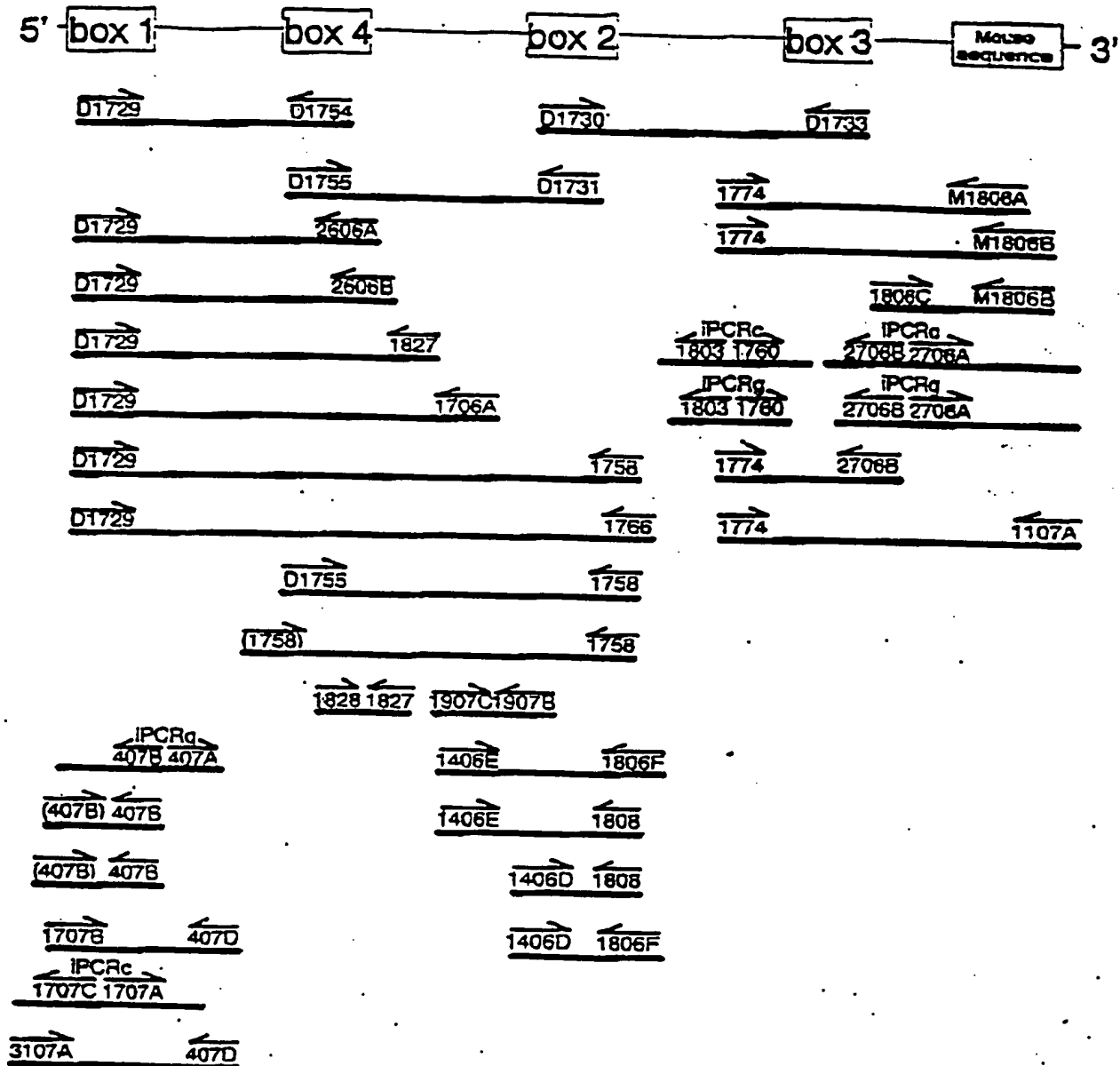
Ec	(1095)	LAEAFAEYLH	(SEQ ID NO:15)
Ss	(1085)	MAEALAEWTH	(SEQ ID NO:16)
Ml1	(56)	LTEALAEYWH	(SEQ ID NO:17)
Hi	(490)	LAEAMAEYLH	(SEQ ID NO:18)
Ce	(1084)	LAEAYAEYLH	(SEQ ID NO:19)
Hs	(1133)	LAEAFAEELH	(SEQ ID NO:20)

**BOX 4:**

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Ec	(262)	GGCCGTPQHI	(SEQ ID NO:21)
Ss	(243)	GGCCGTRPDHI	(SEQ ID NO:22)
Ml2	(226)	GGCCGTPDHI	(SEQ ID NO:23)
Ce	(264)	GGCCGTPDHI	(SEQ ID NO:24)
Hs	(321)	GGCCGSTPDHI	(SEQ ID NO:25)

FIG. 2



**FIG. 3:** Methionine Synthase cDNA (SEQ ID NO: 1) and amino acid (SEQ ID NO: 2) sequences.

GGTCACCTGTGGAGAGCACGTCTTCTCTGCCGCGCCCTCTGCGCAAGGAGGAGACTCGACAAC

1 ATGTCACCCGCGCTCCAAGACCTGTGCAACCCGAAGGTCTGAAGAAAACCTGCGGGATGAGATCAATGCCATTCTGCAGAAGAGGATTATGGTGTGGATGGAGGGATGGGGACCATG 40  
M S P A L Q D L S Q P E G L K K T L R D E I N A I L Q K R I M V L D G G M G T M

121 ATCCAGCGGGAGAAAGCTAAACGAAGAACTTTCCGAGGTGAGGAATTTAAAGATCATGCCAGGCCGCTGAAAGGCAACAATGACATTTAAGTATAACTCAGCCTGATGTCAATTACCAA 80  
I Q R E K L N E E H F R G Q E F K D H A R P L K G N N D I L S I T Q P D V I Y Q

241 ATCCATAAGGAATACTTGTCTGGCTGGGGCAGATATCATTGAAACAAATCTTTAGCAGCACTAGTATTGCCAAGCTGACTATGGCCTGAACACTTGGCCTACCGGATGAACATGTGC 120  
I H K E Y L L A G A D I I E T N T F S S T S I A Q A D Y G L E H L A Y R M N M C

361 TCTGCAGGAGTGGCCAGAAAGCTGCCAGGAGGTAACTCTCCAGACAGGAATTAAGAGTTTGTGGCAGGGGCTCTGGGTCCGACTAATAAGACACTCTCTGTGTCCCCATCTGTGGAA 160  
S A G V A R K A A E E V T L Q T G I K R F V A G A L G P T N K T L S V S P S V E

481 AGGCCGGATTATAGGAACATCACATTTGATGAGCTTGTGAAGCATACCAAGAGCAGGCCAAAGGACTTCTGGATGGCGGGTTGATATCTACTCATTGAACTATTTTTGATACTGCC 200  
R P D Y R N I T F D E L V E A Y Q E Q A K G L L D G G V D I L L I E T I F D T A

601 AATGCCAAGGCAGCTTGTTCCTGCACTCCAAATCTTTTTGAGGAGAAATAGCTCCCGGCCTATCTTTATTTAGGGAGCATGTTGATAAAAGTGGCGGACTCTTCCGGACAGACA 240  
N A K A A L F A L Q N L F E E K Y A P R P I F I S G T I V D K S G R T L S G Q T

721 GGAGAGGATTGTCTCAGCTGTCTCATGGAGAACCCTCTGCATGGATTAATGTGCTTTGGGTGCAGCTGAGATGAGACCTTTTATTGAAATATTGAAAATGTACAACAGCC 280  
G E G F V I S H G E P L C I G L N C A L G A A E M R P F I G K C T T A

841 TATGCTCTGTGTTATCCCAATGCAGGTCTTCCCAACACCTTTGGTGACTATGATGAAAGCCTTCTATGATGGCAAGCACCTAAAGGATTTTGTATGGATGGCTTGGTCAATATAGTT 320  
Y V L C Y P N A G L P N T F G D Y D E T P S M M A K H L K D F A M D G L V N I V

961 GGAGGATGCTGTGGGTCAACACCATCATATCAGGGAATGCTGAAGCTGTGAAAAATTGTAAGCCTAGAGTTCCACCTGCCACTGCTTTTGAGGACATATGTTACTGTCTGGTCTA 360  
G G C C G S T P D H I R E I A E A V K N C K P R V P P A T A F E G H M L L S G L

1081 GAGCCCTTCAGGATTGGACCGTACACCACTTTGTTAATCATGGAGAGCGCTGTAATGTGTCAGGATCAAGGAAGTTTGTCTAACTCATCATGGCAGGAACTATGAAGAAGCCTTGTGT 400  
E P F R I G P Y T N F V N I G E R C N V A G S R K F A K L I M A G N Y E E A L C

1201 GTTGCCAAAGTGCAGGTGGAATGGGAGCCAGGTGTTGGATGTCAACATGGATGATGGCATGCTAGATGGTCCAAGTGAATGACCAGATTTTGAACCTTAATTGCTTCCGAGCCAGAC 440  
V A K V Q V E M G A Q V L D V N M D D G M L D G P S A M T R F C N L I A S E P D

1321 ATCCAAAGGTACCTTTGTGCATCGACTCTCCAATTTGCTGTGATTGAAGCTGGGTAAAGTGCTGCCAAGGGAAGTGCATTGTCAATAGCATTAGTCTGAAGGAAGGAGAGGACGAC 480  
I G A A G T S N F A G C I D S N F I E A G C T I V N A G K C I V N S I L S K E G A D D

1441 TTCTTGAGAAGGCCAGGAAGATTAAAGATGAGGCTGCTATGGTGGTCATGGCTTTGATGAAGAAGGACAGGCAACAGAAACAGACACAAAATCAGAGTGTGCCCCGGGCTAC 520  
F L E K A R K I K K Y G A A M V V M A F D E E G Q A T E T D T K I R V C T R A Y

1561 CATCTGCTTGTGAAAAAACTGGGCTTAATCCAATGACATTATTTTTGACCCTAATATCCTAACCTTGGGACTGGAATGGAGGAACACAACCTGTATGCCATTATTTATCCATGCA 560  
H L L V K K L G F N P N D I I F D P N I L T I G T G M E E H N L Y A I N F I H A

1681 ACAAAGTCATTAAAGAAACATTACCTGGAGCCAGAATAAGTGGAGGTCTTCCAACCTTGCTCTCTCTCCGAGGAATGGAAGCCATTTCGAGAAGCAATGCATGGGGTTTTCTTTAC 600  
T K V I K E T L P G A R I S G G L S N L S F S F R G M E A I R E A M H G V F L Y

1801 CATGCAATCAAGTGGCATGGACATGGAGATAGTGAATGCTGGAACCTCCCTGTGTATGATGATATCCATAAGGAACCTCTGCAGCTCTGTGAAGATCTCATCTGGAATAAAGACCCCT 640  
H A I K S G M D E I V N A G A L D K I L K A A L D H K E L L Q L C E D L I W N K D P

1921 GAGGCCACTGAGAAGCTCTACGTTATGCCAGACTCAAGGCACAGGAGGGAAGAAAGTCAATCAGACTGATGAGTGGAGAAATGGCCCTGTGGAAGAAGCCCTTGAGTATGCCCTTGTG 680  
E A T E K L L R Y A Q T Q G T G G K K V I Q T D E W R N G P V E E R L E Y A L V

2041 AAGGGCATTGAAAAACATATTATTGAGGATACTGAGGAAGCCAGGTAAACCAAAAAAATATCCCCGACCTCTCAATATAATTGAAGGACCCCTGATGAATGGAATGAAATTTGTTGGT 720  
K G I E K H I I E D T E E A R L N Q K K Y P R P L N I I E G P L M N G M K I V G

2161 GATCTTTTGGAGCTGAAAAAATGTTTCTACCTCAGGTTATAAAGTCAGCCCGGTTATGAAGAAGGCTGTTGGCCACCTTATCCCTTTCATGGAAAAAGAGAAGAAACAGAGTG 760  
D L F G A G K M F L P Q V I K S A R V M K K A V G H L I P F M E K E R E E T R V

2281 CTTAAGGCACAGTAGAAGAAGAGGCCCTTACAGGGCACCATCGTGCTGGCCACTGTTAAAGGCGACGTGCACGACATAGGCAAGAACATAGTTGGAGTAGTCTTGGCTGCAATAAT 800  
L N G T V E E E D P Y Q G T I V L A T V K G D V H D I G K N I V G V V L G C N N

2401 TTCCGAGTTATTGATTTAGGAGTCATGACTCCATGTGATAAGATACTGAAAGCTGCTTTGACCACAAGCAGATATAATTGGCCTGTGAGGACTCATCTCTTCCCTGGATGAAATG 840  
F R V I D L G V M T P C D K I L K A A L D H K A D I I G L S G L I T P S L D E M

2521 ATTTTGTGTTGCAAGGAAATGGAGAGATTAGCTATAAGGATTCCATTGTTGATTGGAGGAGCAACCACTTCAAAAACCCACACAGCAGTTAAATAGCTCCGAGATACAGTGCACCTGTA 880  
I F V A K E M E R L A I R I P L L I G G A T T S K T H T A V K I A P R Y S A P V

2641 ATCCATGCTCTGGACGCTCCAAGAGTGTGGTGGTGTGTTCCAGCTGTTAGATGAAATCTAAAGGATGAATACTTTGAGGAAATCATGGAAGAATATGAAGATATTAGACAGGACCAT 920  
I H V L D A S K S V V V C S Q L L D E N L K D E Y F E E I M E E Y E D I R Q D H

2761 TATGAGTCTCTCAAGGAGAGGAGATACTTACCCTTAAGTCAAGCCAGAAAAAGTGGTTTCCAAATGGATTGGTGTCTGAACCTCACCCAGTGAAGCCACGTTTATGGGACCCAGGTC 960  
Y E S L K E R R Y L P L S Q A R K S G F Q M D W L S E P H P V K P T F I G T Q V

2881 TTGAAGACTATGACCTGCAGAAGCTGGTGGACTACATTGACTGGAAGCCTTCTTTGATGTCTGGCAGCTCCGGGCAAGTACCCGAATCGAGGCTTCCCAAGATATTTAACGACAAA 1000  
F E D L Y D L Q K L V D Y I D W K P F F D V W Q L R G P N R G F P K I F N K D K

3001 ACAGTAGGTGGAGAGGCCAGGAAGGTCTACGATGATGCCCCACAATATGCTGAACACACTGATTAGTCAAAAGAACTCCGGGCCCGGGGTGTGGTTGGGTTCTGGCCAGCACAGATATC 1040  
T V G G E A R K V Y D D A H N M L N T L I S Q K K L R A R G V V G F W P A Q S I

3121 CAAGACGACATTACCTGTACGACAGGCTGCTGTGCCAGGCTGCAGAGCCCATAGCCACTTCTATGGGTTAAGGCAACAGGCTGAGAAGGACTCTGCCAGCAGCGGACCATACTAC 1080  
Q D D I H L Y A E A A V P Q A A E P I A T F Y G L R Q Q A E K D S A S T E P Y Y

3241 TGCCTCTCAGACTTCATCGCTCCCTTGCAATCTGGCATCCGTGACTACCTGGGCTGTTTGGCTTGGCTGTTTGGGTTAGAAGAGCTGAGCAAGGCCTATGAGGATGATGGTGACGAC 1120  
C L S D F I A P L H S G I R D Y L G L F A V A C F G V E E L S K A Y E D D G D D

3361 TACAGCAGCATCATGGTCAAGGCGCTGGGGGACCGGCTGGCAGAGGCCTTTGCAGAAGAGCTCCATGAAAGAGTTGCGCGAGAAGTGTGGGCTACTGTGGCAGTGAGCAGCTGGACGTC  
Y S S I M V K A L G D R L A E A F A E E L H E R V R R E L W A Y C G S E Q L D V 1160

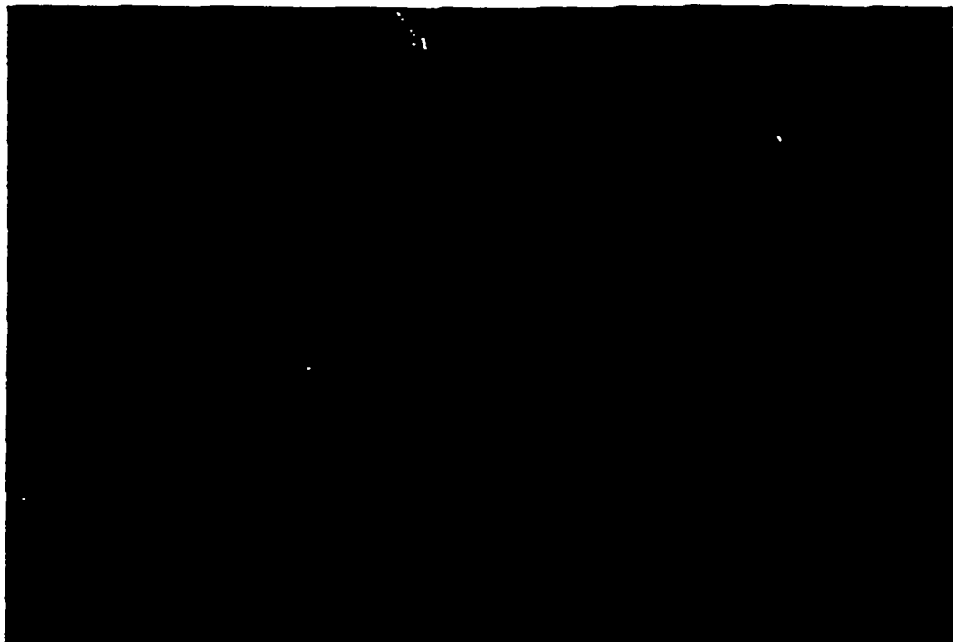
3481 GCAGACCTGCCAAGGTTGCGGTACAAGGCGATCCGCCCCGGCTCCTGGCTACCCAGCCAGCCCGACCACCCGAGAAGCTCACCATGTGGAGACTCGCAGACATCGAGCAGTCTACAGGC  
A D L R R L R Y K G I R P A P G Y P S Q P D H T E K L T M W R L A D I E Q S T G 1200

3601 ATTAGGTTAACAGAATCATTAGCAATGGCACCTGCTTCAGCAGTCTCAGGCCTCTACTTCTCCAATTTGAAGTCCAAATATTTTGCTGTGGGGAAGATTTCCAAGGATCAGGTTGAGGAT  
I R L T E S L A M A P A S A V S G L Y F S N L K S K Y F A V G K I S K D Q V E D 1240

3721 TATGCATTGAGGAAGAACATATCTGTGGCTGAGGTTGAGAAATGGCTTGACCCATTTTGGGATATGATACAGACTAACTTTTTTTTTTTTTTTGCCTTTTTTATCTTGATGATCCTCA  
Y A L R K N I S V A E V E K W L G P I L G Y D T D - 1265

3841 AGGAAATACAACCTAG

FIG. 4



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[illegible]

Detailed description: This is a black and white photograph of a gel electrophoresis result. The gel has four lanes, each labeled with a 'C' at the bottom. To the left of the first two lanes, there are molecular weight markers labeled '7892' and '398'. At the top of the gel, '(bp)' indicates the unit is base pairs. In the fourth lane from the left, an arrow points to a specific band.

[illegible]

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FIG. 6

box 2

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Ec IATVKGDVHDIGKNIVGVVLQCNNEYIVDLGVMVPAEKILRTAKEVNADL

Hi IATVKGDVHDIGKNIVSVVMQCNNEVIDLGVMVPADKIIQTAINQKTDI

Ce IATVKGDVHDIGKNIVSVVLGCNNFKVVDLGVMTPCENIIKAAIEEKADF

Ml LATVKGDVHDIGKNLVDIILSNNGYEVVNLGIKQPITNILEVAEDKSADV

Ss IATVKGDVHDIGKNLVDIILSNNGYRVVNLGIKQPVENII EAYKKHRPDC

Mm LATVKGDVHDIGKNIVGVVLACNNFRVIDLGVMTPCDKILQAALDHKADI

Hs LATVKGDVHDIGKNIVGVVLGCNNFRVIDLGVMTPCDKILKAALDHKADI

...\*\*\*. \* \* . . . . \*...\*\*\* . . . \*

Ec IGLSGLITPSLDEMNVNAKEMERQG--FTIPLLIGGATTSKAHTAVKIEQNY

Hi IALSGLITPSLDEMEYFLGEMTRLG--LNLPMIGGATTSKHTAIKLYPKY

Ce IGLSGLITPSLDEMVIYVAKEMNRVG--LNIPLLIGGATTSKTHTAVKISPRY

Ml VGMSGLLVKSTVIMKENLEEMNTRGVAEKFPVLLGGAALTRSYVENDLAEVY

Ss IAMSGLLVKSTAFMKENLEVFNQEG--ITVPVILGGAALTPKFVHQDCQNTY

Mm IGLSGLITPSLDEMI FVAKEMERLA--IKIPLLIGGATTSRHTAVKIAPRY

Hs IGLSGLITPSLDEMI FVAKEMERLA--IRIPLLIGGATTSKTHTAVKIAPRY

Mutations: Δ

. \* . . . .

Ec -SGPTVYVQNASRTVGVAALLSDTQR--DDFVARTRKEYETVRIQHGRKKP

Hi KQHCVFYTSNASRAVTVCATLMNPEGR--AALWEQFKKDYEKIQQSFANSKP

Ce -PHPVVHCLDASKSVVVCSSLSDMSVR--DAFLQDLNEDYEDVRQEHYASLK

Ml -EGEVHYARDAFEGCLKLMDTIMSAK-RARRCAGEPGVLSRSPQ

Ss -KGQVIYGKDAFADLHFMDKLMPAKNSHNWDDF-QGFLGEYATE-NGHNVTTD

Mm -SAPVIHVLDASKSVVVCSQLLDENLR--DDYLEEILEEYEDIRQDHYESLK

Hs -SAPVIHVLDASKSVVVCSQLLDENLK--DEYFEEIMEEYEDIRQDHYESLK

Mutations: GD

Ec (SEQ ID NO: 73)

Hi (SEQ ID NO: 72)

Ce (SEQ ID NO: 71)

Ml (SEQ ID NO: 70)

Ss (SEQ ID NO: 69)

Mm (SEQ ID NO: 68)

Hs (SEQ ID NO: 67)